

TECH CENTER 1600/2900

AUG 16 2001

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1652

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/488,265

DATE: 07/19/2001

TIME: 16:47:33

Input Set : A:\5808.200-US(sequence).ST25.txt

Output Set: N:\CRF3\07192001\I488265.raw

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3 <110> APPLICANT: Lehmann, Martin
 4 Lassen, Soren F
 6 <120> TITLE OF INVENTION: Improved Phytases
 8 <130> FILE REFERENCE: 5808.200-US
 10 <140> CURRENT APPLICATION NUMBER: 09/488265
 11 <141> CURRENT FILING DATE: 2000-01-20
 13 <160> NUMBER OF SEQ ID NOS: 98
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 440
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Aspergillus terreus 9A-1
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 28 Glu Leu Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln
 29 20 25 30
 32 Asp Glu Ser Pro Phe Pro Leu Asp Val Pro Glu Asp Cys His Ile Thr
 33 35 40 45
 36 Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr His Ser
 37 50 55 60
 40 Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Ser Ala
 41 65 70 75 80
 44 Thr Ala Phe Pro Gly Lys Tyr Ala Phe Leu Gln Ser Tyr Asn Tyr Ser
 45 85 90 95
 48 Leu Asp Ser Glu Glu Leu Thr Pro Phe Gly Arg Asn Gln Leu Arg Asp
 49 100 105 110
 52 Leu Gly Ala Gln Phe Tyr Glu Arg Tyr Asn Ala Leu Thr Arg His Ile
 53 115 120 125
 56 Asn Pro Phe Val Arg Ala Thr Asp Ala Ser Arg Val His Glu Ser Ala
 57 130 135 140
 60 Glu Lys Phe Val Glu Gly Phe Gln Thr Ala Arg Gln Asp Asp His His
 61 145 150 155 160
 64 Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Ala Ile Pro Glu
 65 165 170 175
 68 Gly Ser Ala Tyr Asn Asn Thr Leu Glu His Ser Leu Cys Thr Ala Phe
 69 180 185 190
 72 Glu Ser Ser Thr Val Gly Asp Asp Ala Val Ala Asn Phe Thr Ala Val
 73 195 200 205
 76 Phe Ala Pro Ala Ile Ala Gln Arg Leu Glu Ala Asp Leu Pro Gly Val
 77 210 215 220
 80 Gln Leu Ser Thr Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
 81 225 230 235 240
 84 Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
 85 245 250 255
 88 Asp Leu Phe Thr Ala Thr Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
 89 260 265 270

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92 Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val
93      275      280      285
96 Gln Gly Val Gly Trp Ala Asn Glu Leu Met Ala Arg Leu Thr Arg Ala
97      290      295      300
100 Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Ser Pro
101 305      310      315      320
104 Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
105      325      330      335
108 Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
109      340      345      350
112 Ala Pro Leu Ser Gln Thr Ser Val Glu Ser Val Ser Gln Thr Asp Gly
113      355      360      365
116 Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu
117      370      375      380
120 Met Met Gln Cys Arg Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
121 385      390      395      400
124 Asn Asp Arg Val Met Pro Leu His Gly Cys Pro Thr Asp Lys Leu Gly
125      405      410      415
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137 <211> LENGTH: 440
138 <212> TYPE: PRT
139 <213> ORGANISM: Aspergillus terreus cbs
141 <400> SEQUENCE: 2
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147 Glu Leu Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln
148      20      25      30
151 Asp Glu Ser Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr
152      35      40      45
155 Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser
156      50      55      60
159 Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala
160 65      70      75      80
163 Thr Ala Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser
164      85      90      95
167 Met Gly Ser Glu Asn Leu Thr Pro Phe Gly Arg Asn Gln Leu Gln Asp
168      100     105     110
171 Leu Gly Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile
172      115     120     125
175 Asn Pro Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala
176      130     135     140
179 Glu Lys Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His
180 145     150     155     160
183 Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu
184      165     170     175

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187 Gly Thr Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe
188           180           185           190
191 Glu Ala Ser Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val
192           195           200           205
195 Phe Ala Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val
196           210           215           220
199 Gln Leu Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
200 225           230           235           240
203 Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
204           245           250           255
207 Asp Leu Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
208           260           265           270
211 Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Asn Pro Leu Gly Pro Val
212           275           280           285
215 Gln Gly Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
216           290           295           300
219 Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro
220 305           310           315           320
223 Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
224           325           330           335
227 Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
228           340           345           350
231 Lys Pro Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly
232           355           360           365
235 Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu
236           370           375           380
239 Met Met Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val
240 385           390           395           400
243 Asn Asp Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly
244           405           410           415
247 Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ala
248           420           425           430
251 Gly Gly Asn Trp Ala Glu Cys Phe
252           435           440
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 441
257 <212> TYPE: PRT
258 <213> ORGANISM: Aspergillus niger var. awamori
260 <400> SEQUENCE: 3
262 Asn Gln Ser Thr Cys Asp Thr Val Asp Gln Gly Tyr Gln Cys Phe Ser
263 1           5           10           15
266 Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
267           20           25           30
270 Asn Glu Ser Ala Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
271           35           40           45
274 Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
275           50           55           60
278 Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
279 65           70           75           80

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282 Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
283      85      90      95
286 Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
287      100      105      110
290 Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
291      115      120      125
294 Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
295      130      135      140
298 Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
299 145      150      155      160
302 Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
303      165      170      175
306 Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
307      180      185      190
310 Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
311      195      200      205
314 Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
315      210      215      220
318 Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
319 225      230      235      240
322 Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
323      245      250      255
326 Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Gln Ser
327      260      265      270
330 Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
331      275      280      285
334 Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
335      290      295      300
338 Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
339 305      310      315      320
342 Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
343      325      330      335
346 Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
347      340      345      350
350 Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
351      355      360      365
354 Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
355      370      375      380
358 Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
359 385      390      395      400
362 Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Ile Asp Ala Leu Gly
363      405      410      415
366 Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe Ala Arg Ser
367      420      425      430
370 Gly Gly Asp Trp Ala Glu Cys Ser Ala
371      435      440
374 <210> SEQ ID NO: 4
375 <211> LENGTH: 441
376 <212> TYPE: PRT

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377 <213> ORGANISM: Aspergillus niger T213

379 <400> SEQUENCE: 4

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382 1 5 10 15
385 Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
386 20 25 30
389 Asn Glu Ser Val Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
390 35 40 45
393 Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
394 50 55 60
397 Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
398 65 70 75 80
401 Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
402 85 90 95
405 Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
406 100 105 110
409 Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
410 115 120 125
413 Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
414 130 135 140
417 Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
418 145 150 155 160
421 Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
422 165 170 175
425 Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
426 180 185 190
429 Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
430 195 200 205
433 Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
434 210 215 220
437 Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
438 225 230 235 240
441 Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
442 245 250 255
445 Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Arg Ser
446 260 265 270
449 Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
450 275 280 285
453 Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
454 290 295 300
457 Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
458 305 310 315 320
461 Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
462 325 330 335
465 Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
466 340 345 350
469 Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
470 355 360 365
473 Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu

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VERIFICATION SUMMARY

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